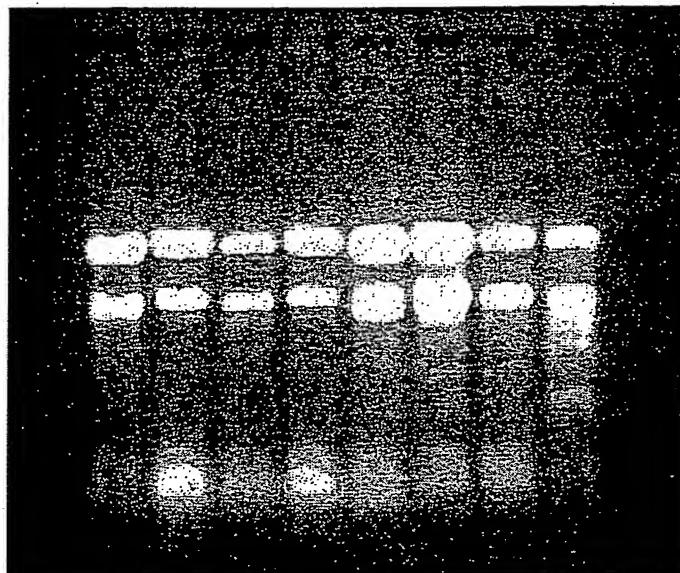


1/15

1 2 3 4 5 6 7 8

A



1 2 3 4 5 6 7 8

B

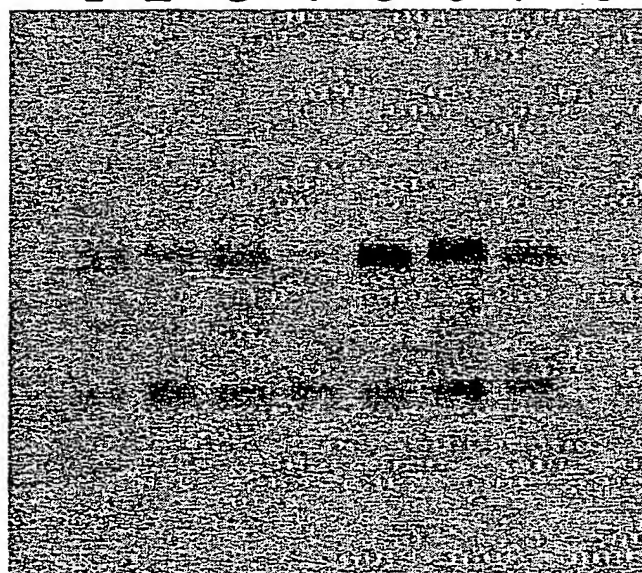


Fig.1

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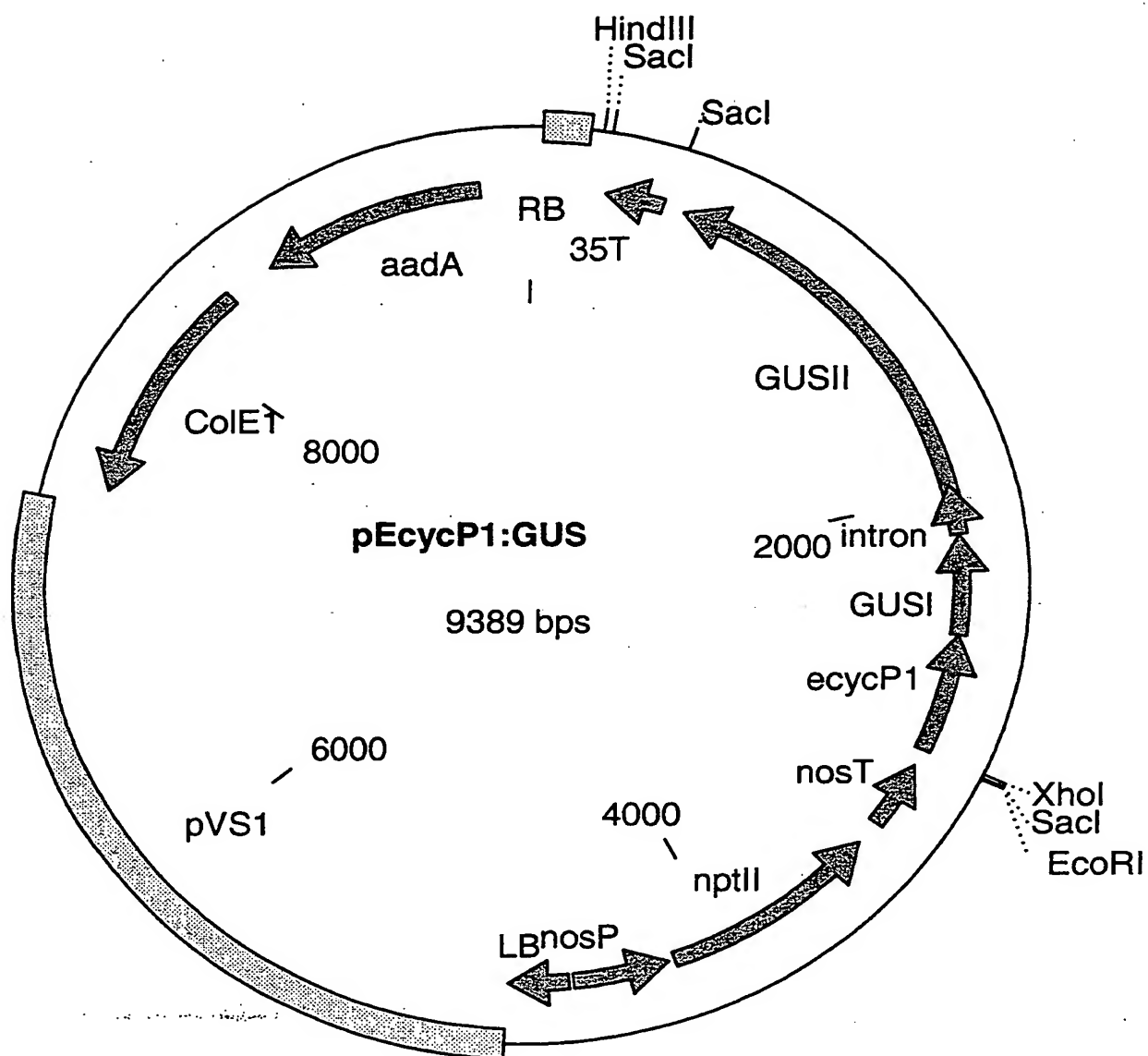


Fig.2

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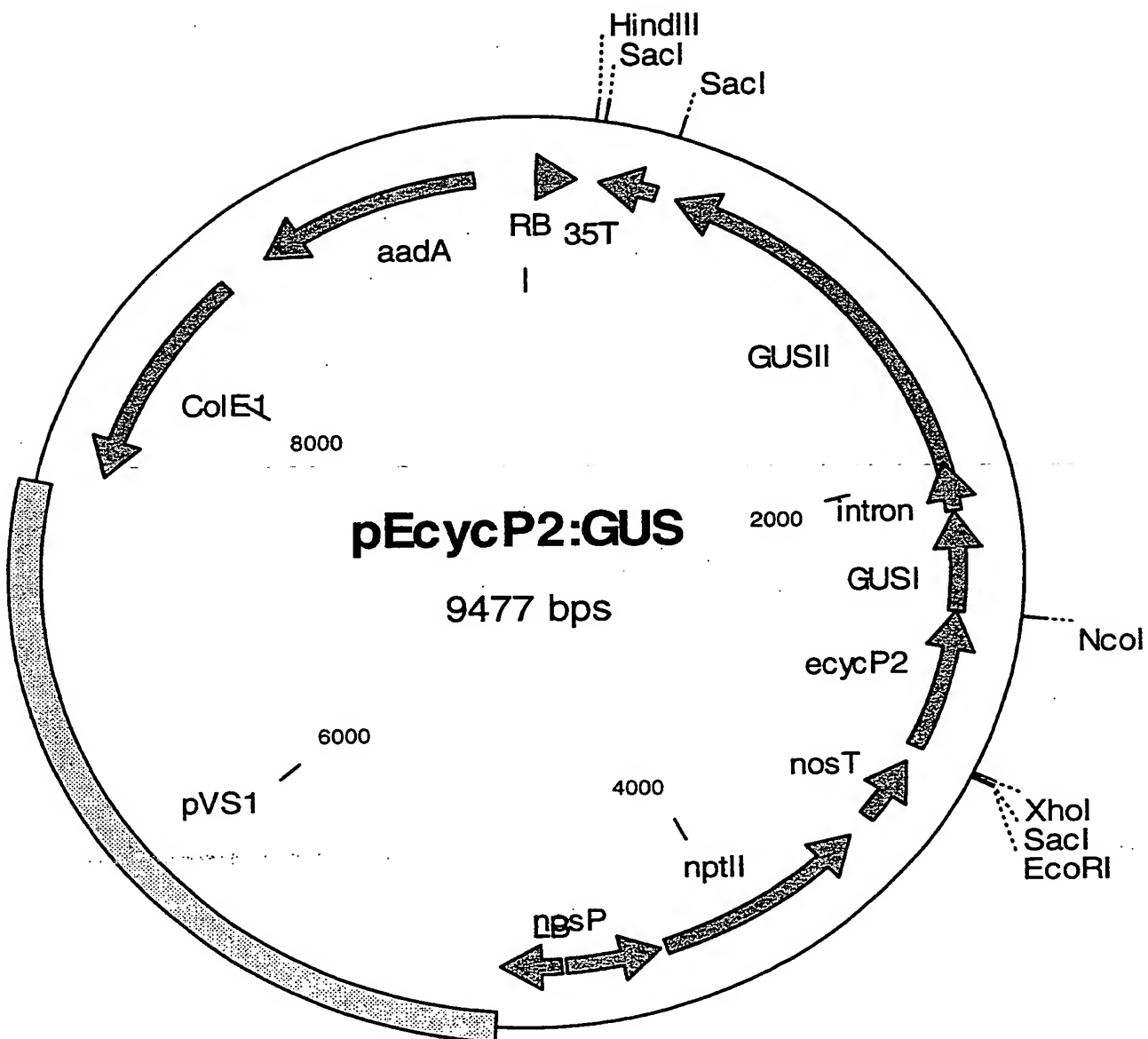


Fig.3

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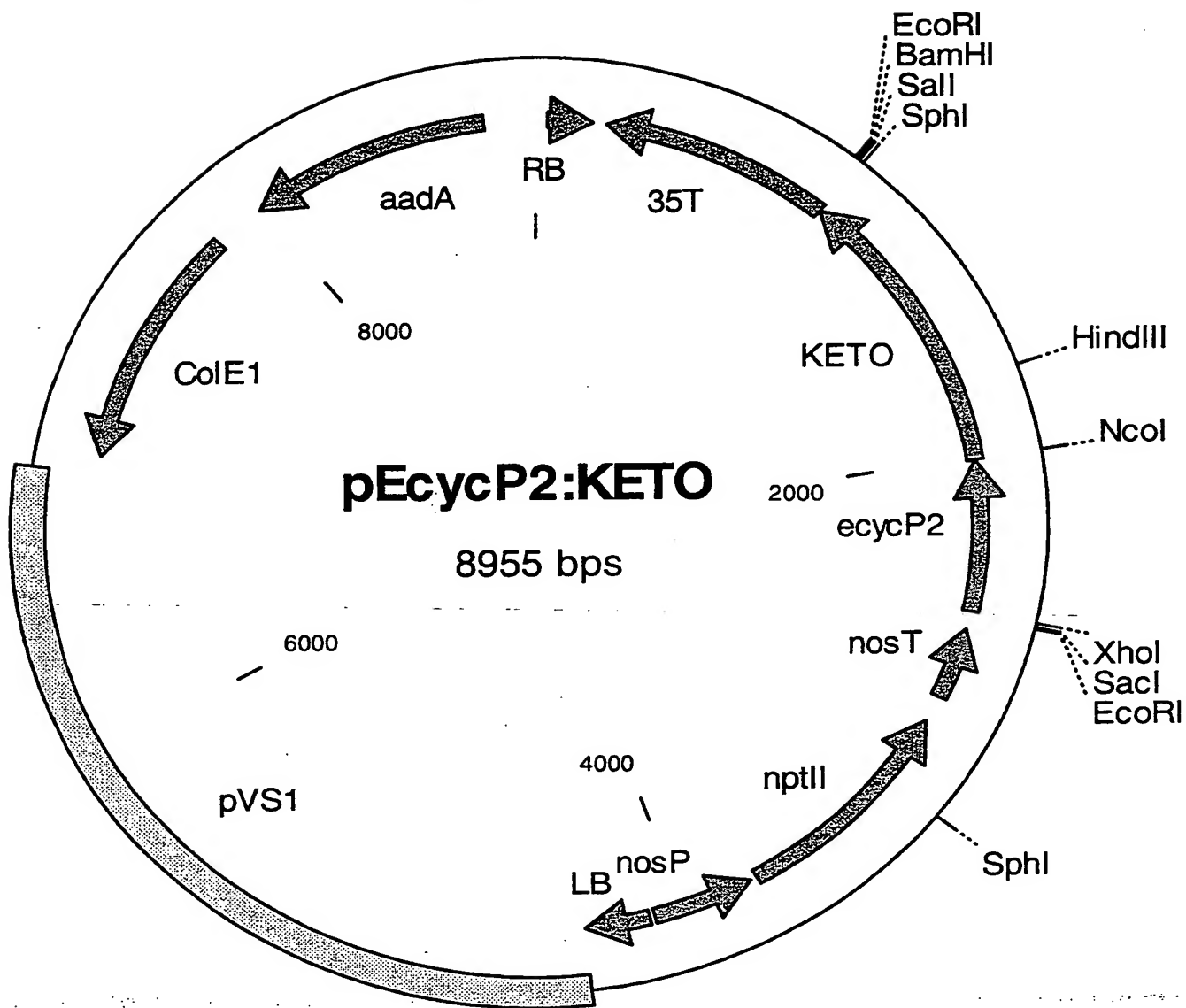


Fig.4

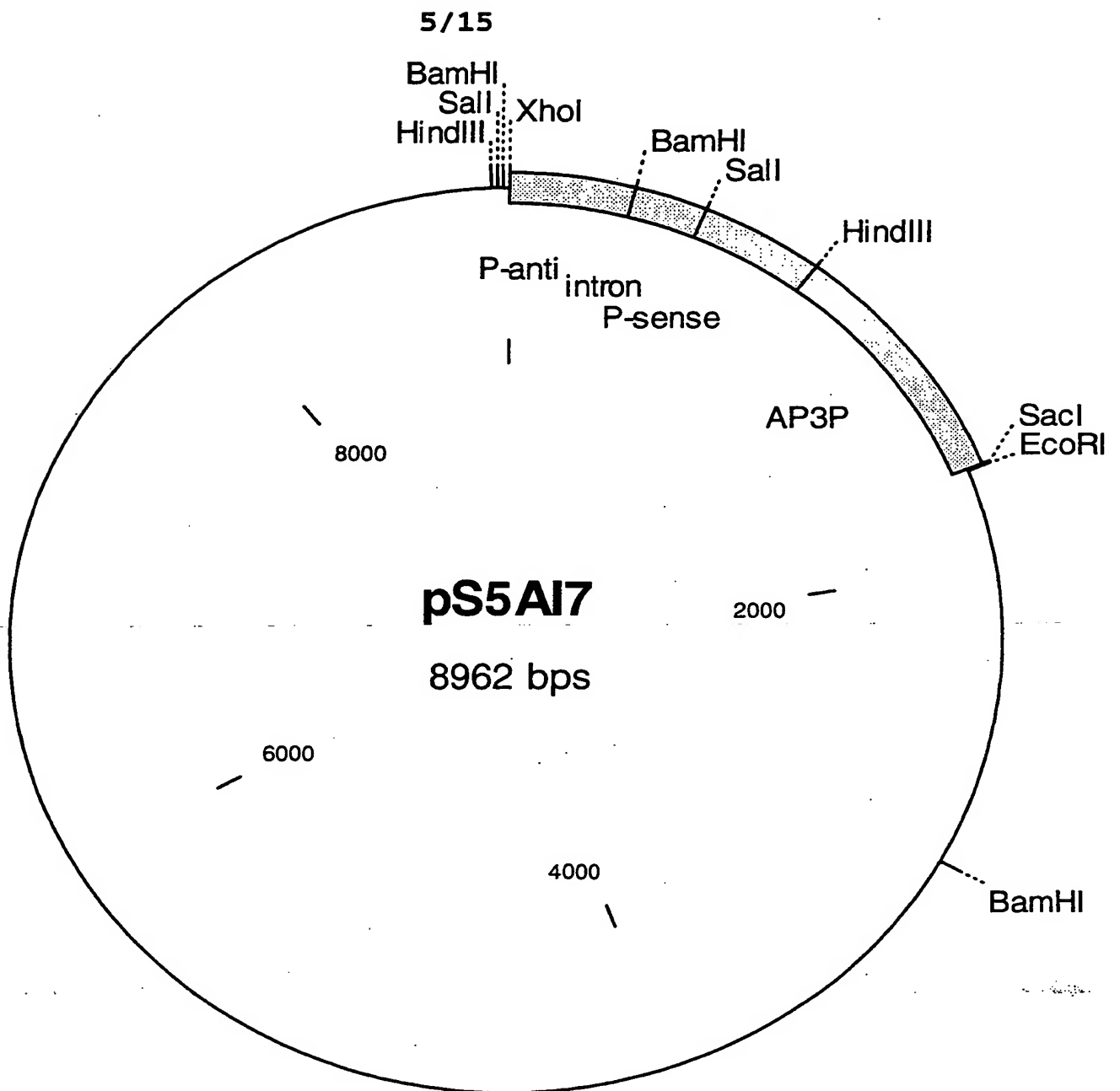


Fig.5

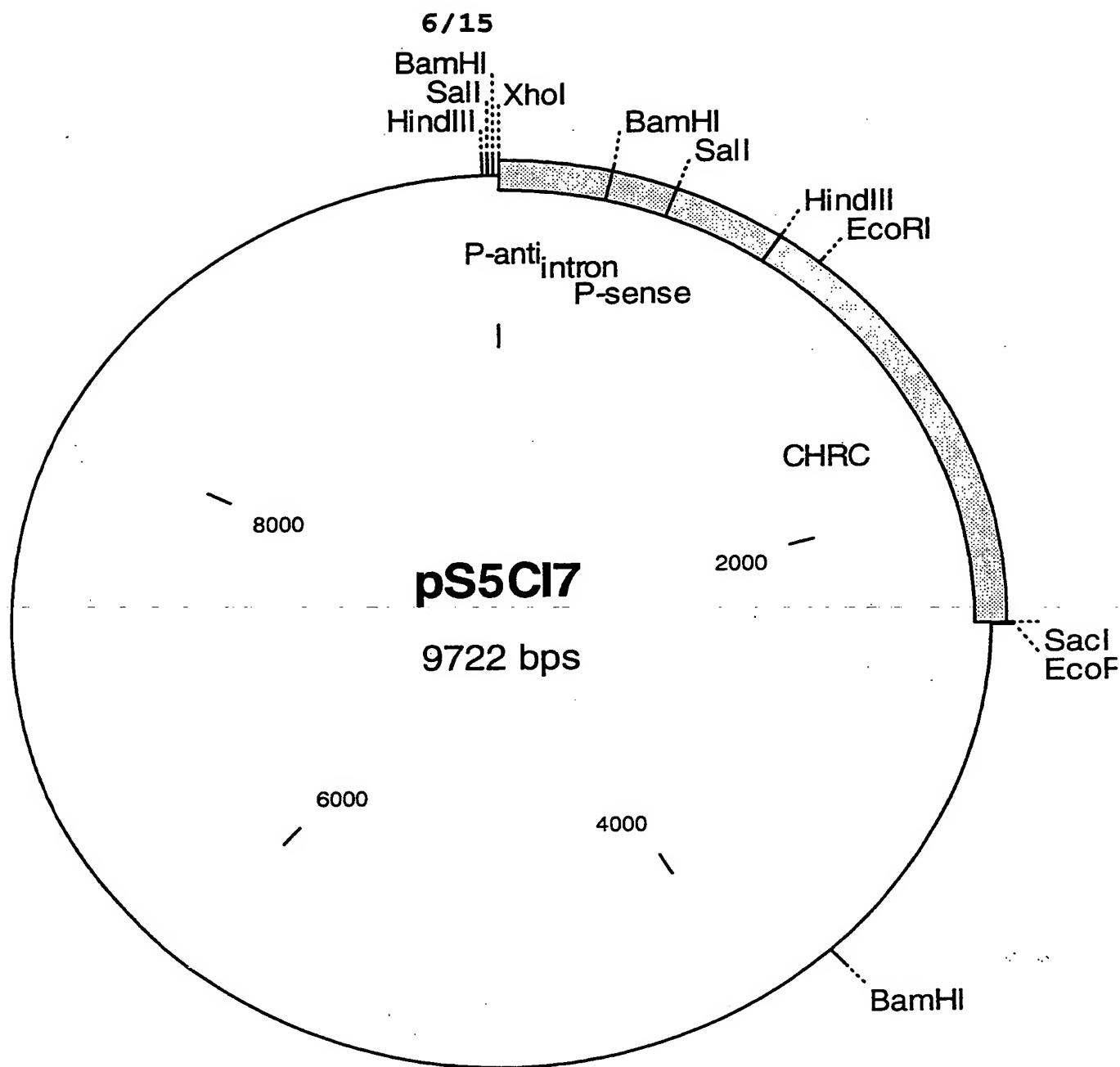


Fig.6

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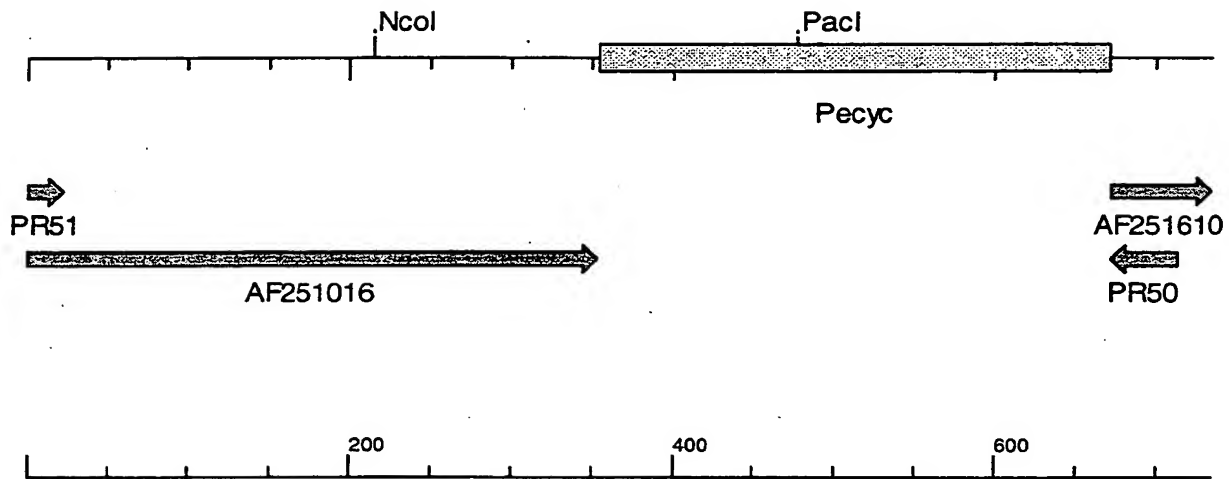
**ecycP-IPCR** (734 bps)

Fig.7

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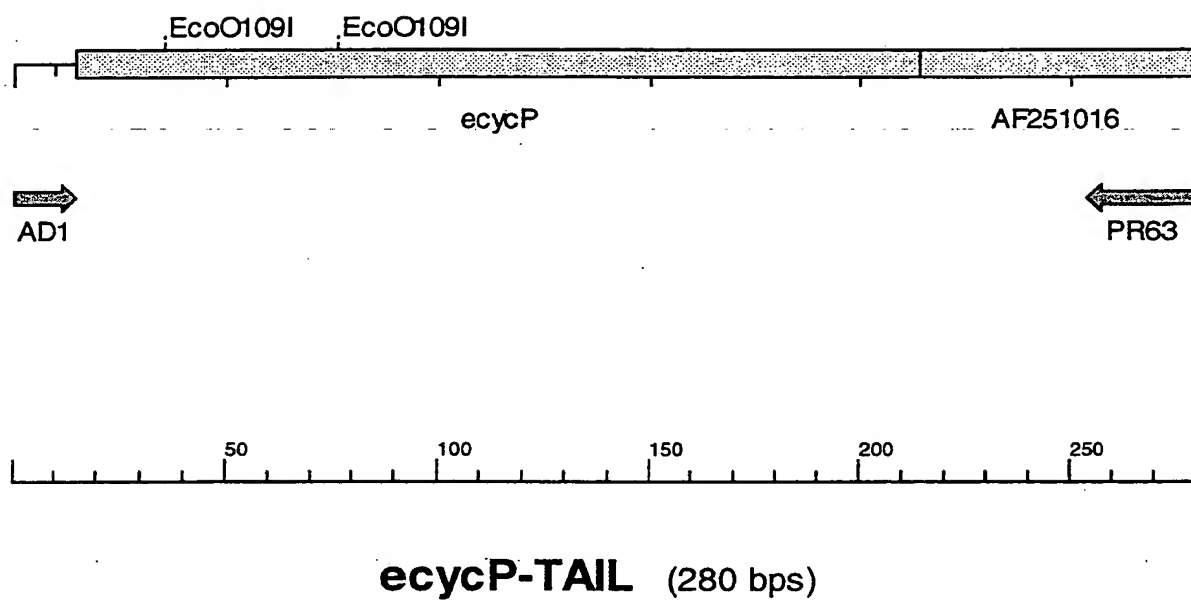


Fig.8

KETO2. seq	ATGCAGCTAGCAGCGACAGTAATGTTGGACGACCTTACCGGAAGCGCTGAGGCACTCAAGGAGAAGGAGAGGTTGCAAGGCACTCTGACGGTGTGC	100
X86782. seq	ATGCAGCTAGCAGCGACAGTAATGTTGGACGACCTTACCGGAAGCGCTGAGGCACTCAAGGAGAAGGAGAGGTTGCAAGGCACTCTGACGGTGTGC	100
KETO2. seq	GTACATGGCGGACCCAGTACTGCGCTTGGTCAGAGGAGTCAGAGCGCGCGCGCGCGGAGCTGAAGAATGCCCTACAAGCCACCACTTCCGACACAAGGG	200
X86782. seq	GTACATGGCGGACCCAGTACTGCGCTTGGTCAGAGGAGTCAGAGCGCGCGCGCGGAGCTGAAGAATGCCCTACAAGCCACCACTTCCGACACAAGGG	200
KETO2. seq	CATCACAAATGGCGCTAGCTGTTCATGCGCTCCGCGCGGAGTGTCTCCACGCCCATTTTTCAAATCAAGCTTCGGAACCTCCCTGGACAGCTGCACCTGG	300
X86782. seq	CATCACAAATGGCGCTAGCTGTTCATGCGCTCCGCGCGGAGTGTCTCCACGCCCATTTTTCAAATCAAGCTTCGGAACCTCCCTGGACAGCTGCACCTGG	300
KETO2. seq	CTGCGGCGGTGCAGATGCCACAGCTCAGCTGGTTAGCGGACAGCAGCGCTGCTGCACATGGTGTAGTATTCTTTGTCTCTGGAGTTCCTGTACACAGGCC	400
X86782. seq	CTGCGGCGGTGCAGATGCCACAGCTCAGCTGGTTAGCGGACAGCAGCGCTGCTGCACATGGTGTAGTATTCTTTGTCTCTGGAGTTCCTGTACACAGGCC	400
KETO2. seq	TTTTTATCAACAACCATGATGCTATGCATGGCAACCATGCCATGAGAAACAGCCAGCTTAATGACTTCCTGGCCAGAGTATGCCATCTCCCTGTACGCCCTG	500
X86782. seq	TTTTTATCAACAACCATGATGCTATGCATGGCAACCATGCCATGAGAAACAGCCAGCTTAATGACTTCCTGGCCAGAGTATGCCATCTCCCTGTACGCCCTG	500
KETO2. seq	GTTTGATTACAACATGCTGCACCGCAAGCAATTTGGGAGCAACCAACACACACTGGCGAGGTGGCAAGGAAOCCGTGACTTCACAGCGGAAOCCGTGGCAAT	600
X86782. seq	GTTTGATTACAACATGCTGCACCGCAAGCAATTTGGGAGCAACCAACACACACTGGCGAGGTGGCAAGGAAOCCGTGACTTCACAGCGGAAOCCGTGGCAAT	600
KETO2. seq	GTGCGCTGGTTGCCAGCTTCATGTCCAGCTACATGTCCATGTGGCAGTTTGGCGCGCTGGCATGGTGGAGCGGTGCATGCCAGCTCGTGGGTGGCCAA	700
X86782. seq	GTGCGCTGGTTGCCAGCTTCATGTCCAGCTACATGTCCATGTGGCAGTTTGGCGCGCTGGCATGGTGGAGCGGTGCATGCCAGCTCGTGGGTGGCCAA	700
KETO2. seq	TGGCGAAGCTGCTGGTGTTCATGGCGCGCGCGCGCATGCTGTGCGCGCTTCCGCTTGTCTACTTTGGCAAGTACATGCCCGCACAGCCGTGAGCCGTGGCG	800
X86782. seq	TGGCGAAGCTGCTGGTGTTCATGGCGCGCGCGCGCATGCTGTGCGCGCTTCCGCTTGTCTACTTTGGCAAGTACATGCCCGCACAGCCGTGAGCCGTGGCG	800
KETO2. seq	CGCGTCAGGCTCTTCAOCCAGCGGTCATGAACCTGGTGGAGTCCGCGCACTAGCCAGCGGTCCGACCTGGTCAAGCTTCTGAACCTGCTACCACTTCGACCTG	900
X86782. seq	CGCGTCAGGCTCTTCAOCCAGCGGTCATGAACCTGGTGGAGTCCGCGCACTAGCCAGCGGTCCGACCTGGTCAAGCTTCTGAACCTGCTACCACTTCGACCTG	900
KETO2. seq	CACTGGGAGCAACAACCGCTGGCCCTTTGGCCCTGGTGGAGCTGGCCAACTGGCCCGCCCTGTCTGGCCGAGGTCGTGGTTCCTGGCTAG	990
X86782. seq	CACTGGGAGCAACAACCGCTGGCCCTTTGGCCCTGGTGGAGCTGGCCAACTGGCCCGCCCTGTCTGGCCGAGGTCGTGGTTCCTGGCTAG	990

Fig. 9

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KETO2.pro	MQLAATVMLEQLTGSAEALKEKEKEVAGSSDVLRTWATQYSLPSEESDAA	50
X86782.pro	MQLAATVMLEQLTGSAEALKEKEKEVAGSSDVLRTWATQYSLPSEESDAA	50
KETO2.pro	RPGLKNAYKPPPSDTKGI TMALAVI GSWAAVFLHAI FQI KLPTSLDQLHW	100
X86782.pro	RPGLKNAYKPPPSDTKGI TMALRVI GSWAAVFLHAI FQI KLPTSLDQLHW	100
KETO2.pro	LPVSDAT AQLVSGSSSLLHI VVVVFFVLEFLYTGLFI TTHDAMHGTI AMRN	150
X86782.pro	LPVSDAT AQLVSGTSSLLDI VVVVFFVLEFLYTGLFI TTHDAMHGTI AMRN	150
KETO2.pro	RQLNDFLGRVCI SLYAWFDYNNMLHRKHWEHHNHTGEVGKDPDFHRGNPGI	200
X86782.pro	RQLNDFLGRVCI SLYAWFDYNNMLHRKHWEHHNHTGEVGKDPDFHRGNPGI	200
KETO2.pro	VPWFASFMSYMSMWQFARLAWWT VVMQLLGAPMANLLVFMAAAPILSAF	250
X86782.pro	VPWFASFMSYMSMWQFARLAWWT VVMQLLGAPMANLLVFMAAAPILSAF	250
KETO2.pro	RLFYFGTYMPHKPEPGAAAGSSSPA VMNWWKSRTSQA SSDLV SFLTCYHFDL	300
X86782.pro	RLFYFGTYMPHKPEPGAAAGSSSPA VMNWWKSRTSQA SSDLV SFLTCYHFDL	300
KETO2.pro	HWEHHRWPFA PWWE L PNCRRRLSGRGLVPA	329
X86782.pro	HWEHHRWPFA PWWE L PNCRRRLSGRGLVPA	329

Fig.10

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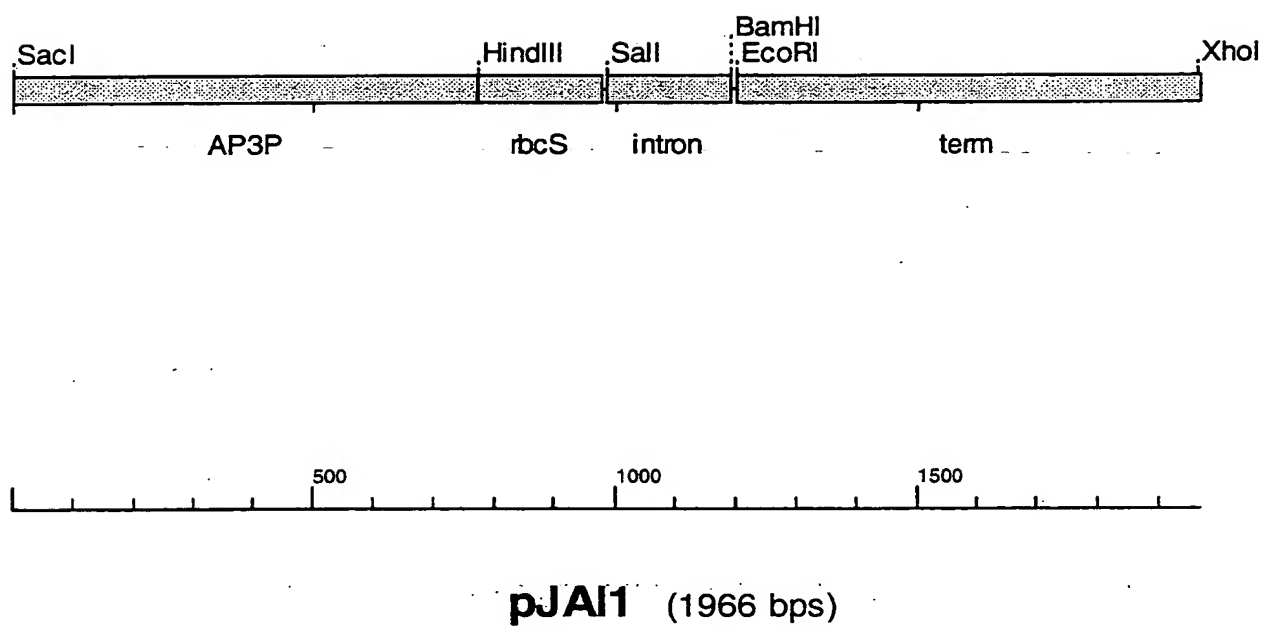


Fig.11

	1	10	20	30	40	50	60	70	80	90	100
A	(1)	MLPFLSSLLNGVTDNPCRKAMDITLLKTHINKLEFLPQVHGALEKS	---	SSLSLKIQIQNELRFGLKKSRQNRNSCFIKASSSALLELPEVETKK	---	---	---	---	---	---	---
B	(1)	---	---	---	---	---	---	---	---	---	---
C	(1)	---	---	---	---	---	---	---	---	---	---
D	(1)	---	MSMRAG	---	HMTATMAAFTCPFRMTS	---	---	---	---	---	---
E	(1)	---	MELLGVR	---	NLISSCPVMIFGIRNLSSSKLAVNTHRYG	---	---	---	---	---	---
F	(1)	---	MELLGVR	---	NLISSCPVMIFGIRNLSSSKLAVNTHRYG	---	---	---	---	---	---
G	(1)	---	---	---	---	---	---	---	---	---	---
H	(1)	---	MECTGAR	---	NMTATMAVFTCPFRFTDCNIRHKFSLLKQRRFTNL	---	---	---	---	---	---
I	(1)	---	---	---	---	---	---	---	---	---	---
J	(1)	---	---	---	---	---	---	---	---	---	---
K	(1)	---	---	---	---	---	---	---	---	---	---
L	(1)	---	---	---	---	---	---	---	---	---	---
M	(1)	---	---	---	---	---	---	---	---	---	---
N	(1)	---	---	---	---	---	---	---	---	---	---
O	(1)	---	---	---	---	---	---	---	---	---	---
P	(1)	---	---	---	---	---	---	---	---	---	---
Consensus	(1)	---	---	---	---	---	---	---	---	---	---

	101	110	120	130	140	150	160	170	180	190	200
A	(101)	---	ENLEFELPMYDPSK	---	GLWDLAVVGGPAGLAVAQVSGAGLSVCSIDPSKLTWNNYGMWVDEFEAMDLLCLDTWSGAVVHIDNITKK	---	---	---	---	---	---
B	(91)	---	---	---	---	---	---	---	---	---	---
C	(1)	---	---	---	---	---	---	---	---	---	---
D	(69)	---	SMDAQSSLSQKLPVPIGGGDSNCILDLVWIGGPAGLALAGESAKLGINVALIG	---	---	---	---	---	---	---	---
E	(87)	---	SMEKQAKLADKLPPIPG	---	---	---	---	---	---	---	---
F	(87)	---	SMEKQAKLADKLPPIPG	---	---	---	---	---	---	---	---
G	(1)	---	---	---	---	---	---	---	---	---	---
H	(92)	---	SMSQSKLSEKLAQIPIG	---	---	---	---	---	---	---	---
I	(1)	---	---	---	---	---	---	---	---	---	---
J	(75)	---	AMDCYSKLSDKLRQISDA	---	---	---	---	---	---	---	---
K	(1)	---	---	---	---	---	---	---	---	---	---
L	(97)	---	SMSQSKLSSKLLPDPEN	---	---	---	---	---	---	---	---
M	(69)	---	SMDAQSSLSQKLPVPIGGGDSNCILDLVWIGGPAGLALAGESAKLGINVALIG	---	---	---	---	---	---	---	---
N	(66)	---	---	---	---	---	---	---	---	---	---
O	(88)	---	DWDEQSKLVKLPPISIG	---	---	---	---	---	---	---	---
P	(85)	---	DMDQSKLSDELRLQISAG	---	---	---	---	---	---	---	---
Consensus	(101)	MD QS LS KLP I G	VLLDLVWIGGPAGLALAGESAKLGL VGLIG	---	---	---	---	---	---	---	---

Fig.12A

(201) 201 210 220 230 240 250 260 270 280 290 300
 A DLNRPYGRVNRKLLKSKMLQKCTINGVKFHQAKVTKVTHEE--SKSLICNDGVITQAAVLDATGFSRCLVQVDKPNP--GYQVAYGILAEVBOHPFDL
 B MIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 C (1) -IGRAYGLVAICFMKNCLKGVSSQVFRILLAQIKRLLKLEWATAMLVKIILSFHAGILILLHLEQLGNPCSMGLGVPEFLSKQIMVSRILRWKPIPYDP
 D (167) LIGRAYGRVSRDILLHEELLJRCMESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 E (180) LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 F (180) LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 G (34) LIGRAYGRVSRHLLHEELLKRCVEAGVLYLNSKVDRLVEATNGHSLVECENNVILPCRFVTVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 H (185) RIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 I (61) LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 J (168) YIGRSYGVSRQILLKELVHRCLESVSYLNKVENINMEGPDGHRVACERGVITPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 K (88) LIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 L (190) MIGRAYGRVSRDILLHEELLJRCMESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 M (167) LIGRAYGRVSRDILLHEELLJRCMESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 N (157) DLSRPYGRVNRKQKSKMLQKCTINGVKFHQAKVTKVTHEE--ANSTVCSGDKVQIQAASVLDATGFSRCLVQVDKPNP--GYQVAYGILAEVBOHPFDL
 O (181) TIGRAYGRVSRHLLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLVECENNVILPCRLATVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 P (178) LIGRAYGRVSRHLLHEELLKRCVEAGVLYLNSKVDRLVEATNGHSLVECENNVILPCRFVTVASGAASEKLLQYELGGPRVSVQIAYGVEVENNNPYDP
 Consensus (201) LIGRAYGRVSR LLHEELLKRCVESGVSYLSKVEKLIIEAGDGHSLV CE I IPCRLATVASGAASEKLL YEVGGPRVSVQIAYGVEVENNNPYDP

(301) 301 310 320 330 340 350 360 370 380 390 400
 A DKMFMMDWRDSDHANNNSQLKEANSKIPITFLYAMPPSSNRIFLEETSIVARPGVPMKDIQERWVARLKHGLGVKSIEED-----EHCVIEMGGPLP
 B (279) SLMVFMMDYRDYTKQKVPQME---AEYPTFLYAMP-----AEYPTFLYAMP-----EHCVIEMGGPLP
 C (100) SLMVFMMDYRDYTKQKVPQME---AEYPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 D (267) SLMVFMMDYRDYTKHKSQSLE---AQYPTFLYAMMSPITKVFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 E (280) NLMVFMMDYRDYTKHKSQSLE---EEYPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 F (280) NLMVFMMDYRDYTKHKSQSLE---EEYPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 G (134) SLMVFMMDYRDYVRHDAQSLE---AKYPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 H (285) DLMVFMMDYRDFSKHKPESLE---AKYPTFLYAMMSPITKVFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 I (161) SLMVFMMDYRDCITKQVPSFE---SINPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 J (268) NVMVFMMDYRDYTKLSVQSLE---AKYPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 K (188) SLMVFMMDYRDCITKQVPSFE---SINPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 L (290) SLMVFMMDYRDCITKQVPSFE---SINPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 M (267) SLMVFMMDYRDCITKQVPSFE---SINPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 N (254) DKMFMMDWRDSDHANNNSQLKEANSKIPITFLYAMPPSSNRIFLEETSIVARPGVPMKDIQERWVARLKHGLGVKSIEED-----EHCVIEMGGPLP
 O (281) DQWFMMDYRDYTKHKSQSLE---AQYPTFLYAMMSPITKVFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 P (278) SLMVFMMDYRDYTKHKSQSLE---AQYPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLLQIMGIRVAKIYEE-----EHSYIPVGGSLP
 Consensus (301) SLMVFMMDYRDYTK KV SLE A YPTFLYAMMSPIRIFFEEHICLASKDAMPFDLLKKKIMSRLL QIMGIRVAKIYEE EHSYIPVGGSLP

Fig.12B

(401) 401 410 420 430 440 450 460 470 480 490 500
 A VLFQRVVGIGGTAGMHPSTGYMVAARTLAAPIVANAIVRSLS--D-----RSISGKLSAEVWKDLWPIERRRQREFFCFQMDILLKLDLPATRFFF
 B (166) -----
 C (188) NTEQKNLAFGAAR-----
 D (355) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPNVAATIAKILGKNSKQMLDHCRYTTN-ISKQAMETIWPLEKRQRRAFFLFGELALIVQMDIEGIRFFF
 E (368) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPKVASVIAKILKQNSAYVVSQSSAVN-ISMQAMSSILWPKERKRQRRAFFLFGELALIVQMDIEATIRFFF
 F (368) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPKVASVIAKILKQNSAYVVSQSSAVN-ISMQAMSSILWPKERKRQRRAFFLFGELALIVQMDIEATIRFFF
 G (222) NTEQKITLAFGAAASWHPATGYSVWRSLSSEAPKCAFVLNLRQNHSHKMLTSS-SIPS-ISTQAMNITLWPKERKRQRSSFFLFGELALILQDIEGIRFFF
 H (373) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPNVAATIAKILRQDQSKEMISLGKVTN--ISKQAMETIWPLEKRQRRAFFLFGELSHVIMDIEGIRFFF
 I (249) NTEQKNLAYGAAS-----
 J (356) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPKVASAIAKILKNDLSKNAILLRQSVGN-ISMQAMNITLWPKERKRQRRAFFLFGELSLIVQDIEGIRFFF
 K (276) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPNVAATIAKILKDHSHRGRLTHQSNEN-ISMQAMNITLWPKERKRQRRAFFLFGELALILQDIEGIRFFF
 L (378) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPRVASVTSIDILNRVYVGEVLPGISQSSPSMLAWRTIWPQERKRQRSSFFLFGELALILQDIEGIRFFF
 M (364) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPNVAATIAKILGKNSKQMLDLGRYTTN-ISKQAMETIWPLEKRQRRAFFLFGELALIVQMDIEGIRFFF
 N (345) VLFQRVVGIGGTAGMHPSTGYMVAARTLAAPIVANAIVRVLGSP-SS-----NSLRGQDLSAEVWRDLWPIERRRQREFFCFQMDILLKLDLDAIRFFF
 O (369) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAPKVASVIAELLREETT-----KQINSN-ISRQAMDTLWPKERKRQRRAFFLFGELALIVQDIEGIRFFF
 P (366) NTEQKITLAFGAAASWHPATGYSVWRSLSSEAPKCAVLANILRQHYSHKMLTSS-SIPS-ISTQAMNITLWPKERKRQRSSFFLFGELALILQDIEGIRFFF
 Consensus (401) NTEQKNLAFGAAASWHPATGYSVWRSLSSEAP YASVIA ILR S L IS QAW TLMP ERKRQRRAFFLFGELALIVQDIEG RFFF

(501) 501 510 520 530 540 550 563
 A DAFFDLERPMHGFSSRLFLPELLVFGLSLFSHASNTSRLEIMAKGTILPLVAMINNLVQDID
 B (166) -----
 C (202) -----
 D (454) RTFFRLPTWMMGFLGSSLSSTDLILFAFYMFIIAPHSLRMGLVRHLLSDPTGGIMLKAYLITI
 E (467) RTFFRLPTWMMGFLGSSLSSTDLVLFSWMMFVLAENSMRMSLVRHLLSDPSGAVMWKAYLER
 F (467) RTFFRLPTWMMGFLGSSLSSTDLVLFSWMMFVLAENSMRMSLVRHLLSDPSGAVMWKAYLER
 G (320) RAFFRVPKMMQGFGLGSSLSXADIMLFAFYMFIIAPNDMRGCLRHLISDPTGATLIRTYLITF
 H (471) RTFFRLPKMMWGFGLGSSLSSTDLILFALYMFVIAPHSLRMELVRHLLSDPTGATMWKAYLITI
 I (263) -----
 J (455) RTFFRVPKMMWGFGLGSSLSADLILFAFYMFIIAPNDLRMGLIRHLLSDPTGATMIRTYLITL
 K (375) RTFFRLPKMMWGFGLGSSLSADLILFAFYMFIIAPNDLRKCLRHLVSDPTGATMWRTYLITL
 L (478) ETFFRLPKMMWGFGLGSSLSVDLILFAFYMFIIAPNQMRMNLVRHLLSDPTGSTMIKTYLITL
 M (463) RTFFRLPTWMMGFLGSSLSSTDLILFAFYMFIIAPHSLRMGLVRHLLSDPTGGIMLKAYLITI
 N (439) DAFFDLQPHYWHGFSSRLFLPELLVFGLSLFSHASNTSRLEIMKGTIVPLAKMINNLVQDRD
 O (462) RTFFRLPKMMQGFGLGSSLSSTDLVLFAFYMFVISPNNLRKGLINHLISDPTGATMIKTYLKV
 P (464) RAFFRVPKMMQGFGLGSSLSADIMLFAFYMFIIAPNDMRGCLRHLISDPTGATLIRTYLITF
 Consensus (501) RTFFRLP WMM GFLGSSLS DLILFA YMFIIAPN ILM LVRHLLSDPTGATMIK YLIT

Fig.12C

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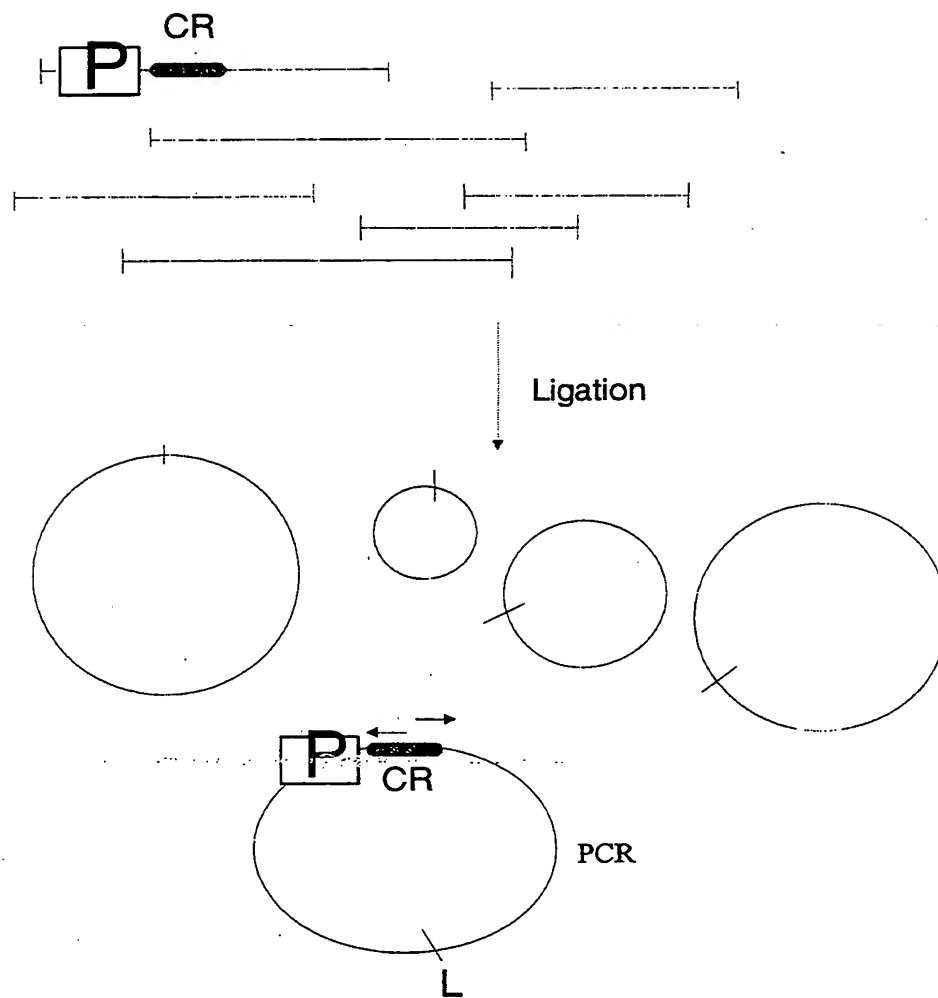


Fig. 13

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